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**I****dentification of** **key genes and** **pathways in** **gastric signet ring cell carcinoma based on transcriptome analysis**

Zhao ZT *et al.* Key genes and pathways to GSRCC

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**Abstract**

BACKGROUND

Gastric signet ring cell carcinoma (GSRCC) is one of the most malignant tumors. It has the features of high invasiveness, rapid progression, and resistance to chemotherapy. However, systematic analyses of mRNAs have not yet been performed for GSRCC.

AIM

To identify key mRNAs and signaling pathways in GSRCC.

METHODS

A transcriptome analysis of two GSRCC and two non-GSRCC samples was performed in this study. Differentially expressed mRNAs and pathways were identified based on the KEGG and PANTHER pathway annotations. The interactive relationships among the differential genes were mapped with the STRING database. Quantitative real-time polymerase chain reaction was used to validate the key gene expression in GSRCC.

RESULTS

About 1162 differential genes (using a 2-fold cutoff, *P* < 0.05) were identified in GSRCC compared with non-GSRCC. The enriched KEGG and PANTHER pathways for the differential genes included immune response pathways, metabolic pathways, and metastasis-associated pathways. Ten genes (*MAGEA2*, *MAGEA2B*, *MAGEA3*, *MAGEA4*, *MAGEA6*, *MUC13*, *GUCA2A*, *FFAR4*, *REG1A*, and *REG1B*) were identified as hub genes in the protein-protein interaction network. The expression levels of five genes (*MAGEA2*, *MAGEA3*, *MAGEA4*, *MAGEA6*, and *REG1B*) showed potential clinical value.

CONCLUSION

We have identified the potential key genes and pathways in GSRCC, and these hub genes and pathways could be diagnostic markers and therapeutic targets for GSRCC.

**Key words:**Signet ring cell; Transcriptome sequencing; Gastric carcinoma; Bioinformatical analysis; Pathway; Gene

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**Core tip:** Gastric signet ring cell carcinoma (GSRCC) is one of the most malignant tumors. It has the features of high invasiveness, rapid progression, and resistance to chemotherapy. However, systematic analyses of mRNAs have not yet been performed for GSRCC. We have identified the potential key genes and pathways of GSRCC, and these hub genes and pathways could be diagnostic markers and therapeutic targets for GSRCC.

**INTRODUCTION**

Gastric cancer (GC) is the 5th most common carcinoma in the world, with a morbidity of over 1000000 new patients in 2018, and is the 3rd principal cause of death by cancer worldwide[1]. Recently, different pathohistological standard methods have been established for GC. The massive majority of GCs are adenocarcinomas, which can be further divided into intestinal and diffuse types by Lauren classification[2,3]. An alternative classification, proposed by the World Health Organization, divides gastric cancer into tubular, mucinous, papillary, and poorly cohesive carcinomas[4]. Diffuse type is generated by poorly cohesive cells without gland formation and is frequently referred to as gastric signet ring cell carcinoma (GSRCC). GSRCC is a histologic diagnosis based on microscopic characteristics as the presence of signet ring cells in over 50% of the cancer cells by the World Health Organization[5]. These classification methods have little clinical value. An important priority of proper classifiers should be studied to guide therapeutics. Considering the epidemiology of GSRCC, it happens more frequently in females than non-GSRCC, and occurs among patients aged between 55 to 61 years, 7 years ahead of those with non-GSRCC[6,7]. Since the beginning of treatment to eradicate *Helicobacter pylori*, the incidence of gastric adenocarcinoma has decreased. Conversely, the incidence of GSRCC is rising. The GSRCC is found in 8% to 30% of GCs[8].

The prognosis of GSRCC in entire mentioned reports has been described as un-inferior than the other gastric cancer subtypes in the early stage[9,10]. Contrariwise, the prognosis of GSRCC in advanced stages is quite poor, and most studies showed a significantly worse 5-year survival rate in patients with GSRCC than in those with non-GSRCC. Furthermore, Lemoine *et al*[11] showed that patients with advanced GSRCC appeared to benefit less from chemotherapy. Pathological response rate to chemotherapy was significantly lower in GSRCC patients (5.3% *vs* 28.1%, *P* = 0.0004). Another German analysis confirmed that a worse histopathological response (16.3% *vs* 28.9%, *P* < 0.001) in patients was affected by preoperative chemotherapy. An ongoing PRODIGE19 trial (NCT01717924) tends to randomize patients with resectable GCs with signet ring cells receiving perioperative chemotherapy with ECF *vs* an upfront surgery followed by adjuvant chemotherapy with the same regimen[12]. However, the results are still uncertain. The effects of chemotherapy on GSRCC are still in controversy. According to its potential drug resistance, current studies have mainly focused on the pathogenesis study of GSRCC with regard to some disease-related genes.

To find out the molecular mechanisms for tumorigenesis and heterogeneity of GSRCC at the molecular level, large studies have been taken to characterize the comprehensive genomic features through transcriptome sequencing, and multiple driver alterations have been recognized. The exploration of the molecular mechanism of GSRCC is important to improve the recognition of GSRCC and find the effective therapeutics to raise the survival rate of patients. To our best knowledge, systematic and comprehensive analyses of mRNAs have not yet been conducted for GSRCC. In this study, transcriptome sequencing and comprehensive analysis were performed to identify key mRNAs and signaling pathways in GSRCC, with an aim to provide new insights into the treatment and feature of GSRCC.

**MATERIALS AND METHODS**

***Gastric signet ring cell cancer tissue samples***

A total of 60 patients who underwent surgery for GSRCC at National Cancer Center, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China were selected for inclusion in the study. All clinicopathological data including age, sex, histological type, and lymph node metastasis were obtained from the database. Four of samples were sent to conduct transcriptome sequencing, and 56 of samples were taken for validation.

***Transcriptome sequencing***

The transcriptome sequencing was used for mRNA expression profiling (CapitalBio).

***KEGG and PANTHER pathway analyses***

The functional enrichment of the differential genes was assessed based on the KEGG and PANTHER pathway annotations.

***Protein-protein interaction network construction***

To evaluate the interactive relationships among the differential genes, we mapped the differential genes to the STRING database (http://string-db.org).

***RNA extraction, RT-PCR, and quantitative real-time PCR***

Total RNA was extracted from frozen fresh tissues with the RNAExpress Total RNA Kit (New Cell & Molecular Biotech Co., Ltd). cDNA was synthesized with the First-Strand cDNA Synthesis Kit (Applied Biological Materials). Quantitative real-time polymerase chain reaction (qPCR) was performed with EvaGreen 2X qPCR MasterMix (Applied Biological Materials). And the primers used are listed in Table 1. The mRNA sequence of *MAGEA2/3/6* is too similar to design primers for separately verifying and validating these three genes, so we designed three pairs of primers for *MAGEA2/3/6* to validate the expression of these genes together.

***Statistical analysis***

The data are presented as the mean ± SE. The differences were assessed by the two-tailed Student's *t*-test for group comparisons using the GraphPad Prism 5 software package. Differences were considered significant when *P*-values were less than 0.05.

**RESULTS**

***Clinical characteristics of SRCC samples***

In this study, four primary GC patients underwent transcriptome sequencing, consisting of two patients with GSRC and two with adenocarcinoma. All of them are male with a median age of 49 years old and poorly differentiated carcinomas. The positive lymph node rate was separately 26/70 and 5/26 in the GSRC group, and 0/45 and 27/34 in the adenocarcinoma group. The two GSRC samples pathologically consisted of over 90% of signet ring cells in the tumor.

Further, 56 samples were chosen for validation. The analysis of the 60 samples showed that there were not significant differences between the GSRCC group and adenocarcinoma group in baseline characteristics such as age, gender, TNM stages, lymphovascular invasion, or nerve invasion, although there were significant differences in Lauren type (*P* < 0.001) and histology differentiation (*P* = 0.038, Table 2).

***Identification of differential genes between GSRCC and non-GSRCC***

Transcriptome sequencing was used to profile the mRNA expression in four patients with GC (two with GSRCC and two with non-GSRCC) who underwent surgical treatment (Figure 1). There were 1162 differential genes (using a 2-fold cutoff, *P* < 0.05), which included 682 upregulated and 480 downregulated genes in GSRCC compared with non-GSRCC. The top 10 up-regulated genes were *MAGEA2*, *MAGEA6*, *MAGEA3*, *MAGEA2B*, *ISY1-RAB43*, *MAGEA9*, *MAGEA9B*, *MAGEA12*, *KRT16P6*, and *NEUROD2*. The top 10 down-regulated genes were *REG1B*, *REG1A*, *SPINK4*, *GIF*, *ATOH1*, *IGHV4-4*, *GUCA2A*, *DMBT1*, *SOSTDC1*, and *ATP4B*. The fold changes and *P*-values of these differential genes are listed in Table 3.

***KEGG and PANTHER pathway enrichment analyses***

KEGG pathway enrichment analyses were performed on the differential genes. The enriched KEGG pathways (Figure 2A) for the differential genes included Rap1 signaling pathway, epidermal growth factor receptor tyrosine kinase inhibitor resistance, antigen processing and presentation, HIF-1 signaling pathway, calcium signaling pathway, PI3K-Akt signaling pathway, inflammatory mediator regulation of TRP channels, phagosome, Ras signaling pathway, gastric acid secretion, metabolic pathways, chemokine signaling pathway, peroxisome proliferator-activated receptors signaling pathway, cytokine-cytokine receptor interaction, and endocytosis. For the differential genes, the enriched PANTHER pathways (Figure 2B) included angiogenesis, apoptosis signaling pathway, epidermal growth factor receptor signaling pathway, Notch signaling pathway, endothelin signaling pathway, inflammation mediated by chemokine and cytokine signaling pathway, vascular endothelial growth factor signaling pathway, glycolysis, fibroblast growth factor signaling pathway, integrin signaling pathway, insulin/insulin like growth factor pathway-protein kinase B signaling cascade, fructose galactose metabolism, CCKR signaling map, interleukin signaling pathway, and Toll receptor signaling pathway. Both KEGG and PANTHER pathways mainly focused on immune response pathways, metabolic pathways, and metastasis-associated pathways.

***Construction and analysis of protein-protein interaction network***

As shown in Figure 3, a regulatory network of differential genes (a 20-fold cutoff, *P* < 0.05) was constructed. There were 141 nodes and 171 edges among these 310 genes. The top 10 hub genes were *MAGEA2*, *MAGEA2B*, *MAGEA3*, *MAGEA4*, *MAGEA6*, *MUC13*, *GUCA2A*, *FFAR4*, *REG1A*, and *REG1B*.

***Validated hub genes in GSRCC with TCGA database and tissue samples***

According to the difference of gene expression and pathway and the protein-protein interaction result, we chose *MAGEA2*, *MAGEA3*, *MAGEA4*, *MAGEA6*, *REG1A*, and *REG1B* for validation. The data of TCGA and GTEx (GEPIA, http://gepia.cancer-pku.cn/index.html) revealed that the expression of *MAGEA2*, *MAGEA3*, *MAGEA4*, and *MAGEA6* was upregulated, but the expression of *REG1B* was downregulated, in GC compared to the normal gastric tissue, and there was no difference in *REG1A* between GC and normal gastric tissues (Figure 4A). The correlation analysis of gene expression and clinical data revealed a negative correlation between *MAGEA2*, *MAGEA3*, *MAGEA4,* and *MAGEA6*, but a positive correlation between *REG1A* and *REG1B*, and poor survival in patients with GC (GEPIA, http://gepia.cancer-pku.cn/index.html, Figure 4B).

To investigate the clinical value of these five genes in GC, qPCR was used to measure their expression in 27 GSRCC and 29 non-GSRCC samples. The qPCR results revealed that the expression of *MAGEA2/3/6* and *MAGEA4* was significantly higher, but the expression of *REG1B* was much lower, in patients with GSRCC than in patients with non-GSRCC (Figure 4C).

**DISCUSSION**

Advanced GSRCC is commonly considered to be more invasive, has a greater probability of lymph node metastasis than other gastric cancer types, has a worse prognosis[13,14], and is less sensitive to chemotherapy than non-SRCC[15-17]. Chemotherapy remains the major treatment for advanced GC. Several studies report that chemoresistance exists in GSRCC with a poor prognosis[8]. It is still unclear whether GSRCC patients can benefit from a detailed therapy.

As we know, vascular endothelial growth factor and HER-2 have been agreed as targets for molecular pathways in GC. However, SRCC cannot benefit from targeted therapy for a low expression level of HER-2[18]. Some studies have mentioned that elevated expression of *PKM2* and *E-cadherin*, and declined expression of *TMEM207* in GSRCC are associated with its biological behavior of invasion and metastasis[19].

Systematic analyses of mRNAs in GSRCC were rare. Chen *et al*[19] reported that hsa-miR-665 and hsa-miR-95 were found in GSRCC compared to intestinal GC, and concluded that these two mRNAs were downregulated in GSRCC but upregulated in intestinal GC, and the relatively differential expression of the miRNAs negatively regulating their target genes could be intently associated with high invasion, metastasis, and chemoresistance of GSRCC[19]. Yao *et al*[20] have described the genome features of GSRCC and they found the importance of highly frequent *CLDN18-ARHGAP26/6* fusions in chemotherapy response in GSRCC. Kakiuchi *et al*[21] reported that *RHOA* mutations happen specifically in diffused GCs, the majority of which were pathologically characterized by the presence of poorly differentiated components, with no available molecularly targeted drugs for this poor-prognosis subtype of GC. However, that study was not specific for GSRCC. Due to a very limited number of studies in this area, this present study aimed to identify specifically expressed genes and identify biological features in GSRCC.

By pathway analyses, we confirmed frequent alterations across various pathways in GSRCC, including immunological response pathways, metabolic pathways, and metastasis-associated pathways. Further protein-protein interaction network analyses identified the hub genes in GSRCC. Of the hub genes, *MAGE-A* family and *REG1B* are immune-related genes. *REG1B* has been reported to be able to upregulate the expression of interleukin (IL)-6 mRNA and protein.

*MAGE-A* family are the best characterized cancer-testis antigens (*CTA*) family members, which are expressed mainly, but not exclusively, in germ cells. *MAGE-A* family are infrequently expressed in the normal human placenta, but they are widely expressed in numerous human cancers. Alvi *et al*[22] concluded that the MSI+/CIMP+/BRAF V600E+/CD3+/PDL1+ hypermethylated genotype is an ideal candidate for immune checkpoint inhibitor therapy. In addition, one-fourth of SRCC cases can potentially be targeted by KIT inhibitors. As similar as we found, MAGE-A proteins are highly immunogenic and are considered as potential targets for immuno-therapy.

In conclusion, we have identified the potential key genes and pathways in GSRCC. These hub genes and pathways could be diagnostic markers and therapeutic targets for GSRCC. *MAGE-A* family as a *CTA* family member may be the potential targets for GSRCC. More research should be conducted for exploration of the mechanisms involved.

**ARTICLE HIGHLIGHTS**

***Research background***

Gastric signet ring cell carcinoma (GSRCC) has the features of high invasiveness, rapid progression, and resistance to chemotherapy. However, systematic analyses of mRNAs have not yet been performed.

***Research motivation***

The exploration of the molecular mechanism of GSRCC is important to improve the recognition of GSRCC and find the effective therapeutics to raise the survival rate of patients.

***Research objectives***

Transcriptome sequencing and comprehensive analysis were performed to identify key mRNAs and signaling pathways in GSRCC.

***Research methods***

A transcriptome analysis of two GSRCC and two non-GSRCC samples was performed. Differentially expressed mRNAs and pathways were identified. The interactive relationships among the differential genes were mapped with the STRING database.

***Research results***

The enriched KEGG and PANTHER pathways for the differential genes included immune response pathways, metabolic pathways, and metastasis-associated pathways. *MAGEA2*, *MAGEA2B*, *MAGEA3*, *MAGEA4*, *MAGEA6*, *MUC13*, *GUCA2A*, *FFAR4*, *REG1A*, and *REG1B* were identified as hub genes in the protein-protein interaction network. The expression levels of *MAGEA2*, *MAGEA3*, *MAGEA4*, *MAGEA6*, and *REG1B* showed potential clinical value.

***Research conclusions***

The potential key genes and pathways of GSRCC have been identified. These hub genes and pathways could be diagnostic markers and therapeutic targets for GSRCC.

***Research perspectives***

*MAGE-A* family as a *CTA* family member may be the potential targets for GSRCC. More research should be conducted for exploration of the mechanisms involved.

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**Footnotes**

**Institutional review board statement:** This study was approved by the institutional review board of the National Cancer Center of China.

**Informed consent statement:** The institutional review board of the National Cancer Center of China waived informed consent due to the retrospective nature of this research.

**Conflict-of-interest statement:** We have no financial relationships to disclose.

**Data sharing statement:** No additional data are available.

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**Figure Legends**

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**Figure 1 Summary of transcriptome sequencing results of mRNA expression in gastric carcinoma.** A: Circos plot shows the differential genes on the human chromosomes. From the outside and inwards, the first layer of the Circos plot is a chromosome map of the human genome; the black and white bars represent expression, while the third layer of circus plot represents differential genes, red indicates up-regulated genes, and green indicates down-regulated genes; B: Volcano plot of the distributions of mRNAs; C: Numbers of differential genes between gastric signet ring cell carcinoma and non-gastric signet ring cell carcinoma; D: Cluster analysis of functional mRNAs in four cases of gastric carcinoma, and data are presented as a heat map (*P* < 0.05). GSRCC: Gastric signet ring cell carcinoma.

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**Figure 2 KEGG and PANTHER pathway analysis of differential genes.** A: Top 15 enriched KEGG pathways are presented; B: Top 15 enriched PANTHER pathways are presented.

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**Figure 3 Protein-protein interaction network of differential genes.** Using the STRING online database, 310 genes were selected and used to construct the protein-protein interaction network.

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**Figure 4 Expression of *MAGEA2/3/6*, *MAGEA4*, and *REG1B* in gastric signet ring cell carcinoma.** Data were collected from TCGA and GTEx data using GEPIA (http://gepia.cancer-pku.cn/index.html). A: FPKM of genes in transcriptome sequencing data in 408 gastric carcinoma tissues (T) and 211 normal tissues (N); B: Survival rate calculated by the Kaplan-Meier method in patients separated according to the median expression level of each gene (95%CI); C: Quantitative real-time PCR was used to measure the relative expression levels of the indicate genes in 27 gastric signet ring cell carcinoma samples and 29 non-gastric signet ring cell carcinoma samples. The results were normalized to the endogenous *GAPDH* RNA control. GSRCC: Gastric signet ring cell carcinoma.

**Table 1 Primers used for quantitative real-time polymerase chain reaction**

|  |  |
| --- | --- |
| **Gene** | **Primer sequence (5’-3’)** |
| *MAGEA2/3/6*; primer 1 | F: CAGAGGAGTCAGCACTGCAA |
| R: TAGTCGAGAAGCTGGAGGCT |
| *MAGEA2/3/6*; primer 2 | F: CAGAGGAGTCAGCACTGCAA |
| R: TAGTCGAGAAGCTGGAGGCT |
| *MAGEA4* | F: CTGCTGTCTCCTCCTCCTCT |
| R: GGAACAAGGACTCTGCGTCA |
| *MAGEA2/3/6*; primer 3 | F:CAGAGGAGTCAGCACTGCAA |
| R:GACTCTGGGGAGGATCTGGT |
| *REG1A* | F: TGACCCCAAAAAGAACCGCC |
| R: AGAACTTGTCTTCACAAGGCAC |
| *REG1B* | F: GATCCCCGAGCAGTGCTAAT |
| R: CTTCTCACAAGATTCATCCTTCCA |
| *GAPDH* | F: TGTTGCCATCAATGACCCCTT |
| R: CTCCACGACGTACTCAGCG |

F: Forward; R: Reverse.

**Table 2 Characteristics of 30 gastric signet ring cell carcinoma and 30 adenocarcinoma patients, *n* (%)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Characteristic** | **Overall (*n* = 60)** | **GSRCC (*n* = 30)** | **Adenocarcinoma (*n* = 30)** | ***P* value** |
| **Age (yr)** |  |  |  | 0.052 |
| ≤ 65 | 41 (68.3) | 24 (80.0) | 17 (56.7) |  |
| > 65 | 19 (31.7) | 6 (20.0) | 13 (43.3) |  |
| **Gender** |  |  |  | 0.584 |
| Male | 40 (66.7) | 21 (70.0) | 19 (63.3) |  |
| Female | 20 (33.3) | 9 (30.0) | 11 (36.7) |  |
| **Tumor size (cm)** |  |  |  | 0.584 |
| ≤ 5 | 40 (66.7) | 21 (70.0) | 19 (63.3) |  |
| > 5 | 20 (33.3) | 9 (30.0) | 11 (36.7) |  |
| Lauren type |  |  |  | **0.000** |
| Intestinal | 12 (20.0) | 0 (0) | 12 (40.0) |  |
| Diffuse | 35 (58.3) | 26 (86.7) | 9 (30.0) |  |
| Mixed | 12 (20.0) | 4 (13.3) | 8 (26.7) |  |
| Unknown | 1 (1.67) | 0 (0) | 1 (3.3) |  |
| **Histology differentiation** |  |  |  | **0.038** |
| Poorly/un-differentiated | 56 (93.3) | 30 (100.0) | 26 (86.7) |  |
| Well/moderately differentiated | 4 (6.7) | 0 (0) | 4 (13.3) |  |
| Unknown |  |  |  |  |
| **T stage** |  |  |  | 0.725 |
| T1 | 5 (8.3) | 3 (10.0) | 2 (6.7) |  |
| T2 | 9 (15.0) | 3 (10.0) | 6 (20.0) |  |
| T3 | 12 (20.0) | 6 (20.0) | 6 (20.0) |  |
| T4 | 34 (56.7) | 18 (60.0) | 16 (53.3) |  |
| **N stage** |  |  |  | 0.639 |
| N0 | 16 (26.7) | 8 (26.7) | 8 (26.7) |  |
| N1 | 6 (10.0) | 3 (10.0) | 3 (10.0) |  |
| N2 | 20 (33.3) | 8 (26.7) | 12 (40.0) |  |
| N3 | 18 (30.0) | 11 (36.7) | 7 (23.3) |  |
| **M stage** |  |  |  | 0.150 |
| Metastasis | 2 (3.3) | 2 (6.7) | 0 (0) |  |
| No metastasis | 58 (96.7) | 28 (93.3) | 30 (100.0) |  |
| **Positive lymph nodes** |  |  |  | 0.390 |
| ≤ 8 | 43 (71.7) | 20 (66.7) | 23 (76.7) |  |
| > 8 | 17 (28.3) | 10 (33.3) | 7 (23.3) |  |
| Lymphovascular invasion |  |  |  | 0.355 |
| Yes | 31 (51.7) | 15 (50.0) | 16 (53.3) |  |
| No | 27 (45.0) | 13 (43.3) | 14 (46.7) |  |
| Unknown | 2 (3.3) | 2 (6.7) | 0 (0) |  |
| Nerve invasion |  |  |  | 0.213 |
| Yes | 42 (70.0) | 22 (73.3) | 20 (66.7) |  |
| No | 16 (26.7) | 6 (20) | 10 (33.3) |  |
| Unknown | 2 (3.3) | 2 (6.7) | 0 (0) |  |
| **Neoadjuvant chemotherapy** |  |  |  | 0.688 |
| Yes | 7 (88.3) | 4 (13.3) | 3 (10.0) |  |
| No | 53 (11.7) | 26 (86.7) | 27 (90.0) |  |

GSRCC: Gastric signet ring cell carcinoma.

**Table 3 Fold change of differential genes**

|  |  |  |
| --- | --- | --- |
| **Genes** | **Fold change** | ***P* value** |
| **Top 10 up-regulated genes** | | |
| *MAGEA2* | 9182.176 | 0.000031 |
| *MAGEA6* | 4410.054 | 0.000429 |
| *MAGEA3* | 2508.358 | 0.0000307 |
| *MAGEA2B* | 1971.738 | 0.0000976 |
| *ISY1-RAB43* | 1921.249 | 0.0000394 |
| *MAGEA9* | 1787.459 | 0.002399 |
| *MAGEA9B* | 1469.006 | 0.001587 |
| *MAGEA12* | 1064.08 | 0.000427 |
| *KRT16P6* | 633.9792 | 0.043469 |
| *NEUROD2* | 574.5342 | 0.000245 |
| **Top 10 down-regulated genes** | | |
| *REG1B* | 0.00000891 | 0.008502 |
| *REG1A* | 0.000149 | 0.004671 |
| *SPINK4* | 0.000217 | 0.009491 |
| *GIF* | 0.000237 | 0.000152 |
| *ATOH1* | 0.000632 | 0.018238 |
| *IGHV4-4* | 0.000822 | 0.0000723 |
| *GUCA2A* | 0.000853 | 0.011982 |
| *DMBT1* | 0.001304 | 0.001651 |
| *SOSTDC1* | 0.001678 | 0.000862 |
| *ATP4B* | 0.001709 | 0.017566 |